



FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastacAAHaihS: 874 aa

>SEQ ID NO: 3 human semaphorin

vs /tmp/fastadAAOHaihS library

searching /tmp/fastadAAOHaihS library

782 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 38, opt: 26, gap-pen: -12/-2, width: 16

Scan time: 0.017

The best scores are:

gi|8978202|dbj|BAA98132.1| semaphorin sem2 [Homo (782) 5450

>>gi|8978202|dbj|BAA98132.1| semaphorin sem2 [Homo sapie (782 aa)

initn: 5448 initl: 4266 opt: 5450

Smith-Waterman score: 5450; 99.872% identity in 782 aa overlap (94-874:1-782)

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SEQ    GGSRRANRRPAGPEGGSAGRRQRCQFSPMAPSAWAICWLLGGLLLHGGSSGSPGPSV
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gi|897      MAPSAWAICWLLGGLLLHGGSSGSPGPSV
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      130     140     150     160     170     180
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gi|897 PRLRLSYRDLLSANRSAIFLGPQGSNLQAMYLDEYRDLFLGGLDALYSLRLDQAWPDP
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      190     200     210     220     230     240
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gi|897 REVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGH
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      250     260     270     280     290     300
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      310     320     330     340     350     360
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gi|897 ALRSDSDQSLLHDPFRVMAARIPENSQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVC
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      370     380     390     400     410     420
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gi|897 VNDAGGQRVLVNKGWSTFLKARLVCSVPGPGGAETHFDQLEDVFLWPKAGKSLEVYALFS
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      430     440     450     460     470     480
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      490      500      510      520      530      540
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gi|897 GRPFGSTKDYPDEVLQFARAHPLMFVPRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGT
      550      560      570      580      590      600
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gi|897 YDVIFLGTDSGSVLKVIALQAGGSAEPPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGS
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SEQ    RLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPA
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gi|897 RLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPA
      670      680      690      700      710      720
SEQ    LQCLGQSQEEEEAVGLVAATMVYGTETNSTFLECLPKSP-AAVRWLLQRPGEDEGPDQVKTD
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gi|897 LQCLGQSQEEEEAVGLVAATMVYGTETNSTFLECLPKSPQAAVRWLLQRPGEDEGPDQVKTD
      730      740      750      760      770      780
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gi|897 ERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPE
      790      800      810      820      830      840
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gi|897 EPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCVWCRGTTECSGCFRSGKQA
      850      860      870
SEQ    RGKSWAGLELGKKMKSRVHAEHNRTPREVEAT
      760      770      780
gi|897 RGKSWAGLELGKKMKSRVHAEHNRTPREVEAT
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874 residues in 1 query sequences

782 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Feb 10 16:12:17 2003 done: Mon Feb 10 16:12:17 2003

Scan time: 0.017 Display time: 0.933

Function used was FASTA



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Bio

 Search for

Limits

Preview/Index

History

Clipboard

Details

Display

Show:

Send to

☐ 1: BAA98132. semaphorin sem2 [...[gi:8978202]

BLink, Domains, Links

LOCUS BAA98132 782 aa linear PRI 07-JUL-2000
 DEFINITION semaphorin sem2 [Homo sapiens].
 ACCESSION BAA98132
 VERSION BAA98132.1 GI:8978202
 DBSOURCE accession AB029496.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 782)
 AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
 Miyajima,N. and Saito,T.
 TITLE Human semaphorin
 JOURNAL Published Only in DataBase (2000)
 REFERENCE 2 (residues 1 to 782)
 AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
 Miyajima,N. and Saito,T.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUL-1999) Toshiyuki Saito, National Institute of
 Radiological Sciences, Genome Research Group; Inage-ku Anagawa
 4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
 Tel:81-43-201-3135, Fax:81-43-251-9818)
 FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:9606"
Protein 1..782
 /product="semaphorin sem2"
CDS 1..782
 /gene="sem2"
 /coded_by="AB029496.1:1..2349"

ORIGIN

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121 rvlqphnrth llacgtgafq ptcalitvgh rgehvlhleph gsvesgrgrc phepsrpfas
181 tfidgelytg ltadflgrea mifrsggprp alrdsdqs1 lhdprfvmaa ripensdqdn
241 dkvyffffset vspdggsnh vtvsrvgrvc vndaggqrvi vnkwtflka rlvcsvpgpg
301 gaethfdgle dvfllwpkag kslevyalfs tvsavfqqfa vcvyhmadiw evfngpfahr
361 dgpqhqwgy py ggvkfprpg vcpskmtaqp grpfgstky pdevlqfara hplmfwpvrp
421 rhgrpvlvkt hlaqqlhqiv vdrveadgt ydviflgt ds gsvlkvialq aggsaepeev
481 vleelqvfkv ptpitemeis vkrqmlyvgs rlgvaqlrlh qcetygtaca ecclardpyc
541 awdgascthy rpslgkrrfr rqrdirhnpa lqclggsqee eavglvaatm vygtehnstf
601 leclpkspqa avrwllqrpq degpdqvkt d ervlhtergl lfrlrsrfa gtytcttleh
661 gfsqtvvrla lvvivasqld nlfppepkpe eppargglas tppkawykd lqligfanlp
721 rvdeycervw crgttecs gc frsrsrgkqa rgkswagel gkkmksrvha ehnrtpreve
781 at

```

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAavaaG8P: 781 aa

>SEQ ID NO: 3 human semaphorin
vs /tmp/fastaHAAwaaG8P library
searching /tmp/fastaHAAwaaG8P library

814 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 38, opt: 26, gap-pen: -12/-2, width: 16
Scan time: 0.034

The best scores are:

SEQ ID NO:1 human semaphorin MACALAGKVFPMSGWPVWHK (814) 5462 opt

>>SEQ ID NO:1 human semaphorin MACALAGKVFPMSGWPVWHKSLHWA (814 aa)

initn: 5462 initl: 5462 opt: 5462

Smith-Waterman score: 5462; 100.000% identity in 781 aa overlap (1-781:34-814)

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                                10      20      30
SEQ                          MAPSAWAICWLLGGLLLHGGSSGSPSPGPSV
                                .....
SEQ  GGSRANYNRRPAGPEGGSAGRRQRCQPFSMAPSAWAICWLLGGLLLHGGSSGSPSPGPSV
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                                40      50      60      70      80      90
SEQ  PRLRLSYRDLLSANRSAIFLGPQGSNLQAMYLDEYRDRLFGLGDLALYSRLDQAWPDP
      .....
SEQ  PRLRLSYRDLLSANRSAIFLGPQGSNLQAMYLDEYRDRLFGLGDLALYSRLDQAWPDP
      70      80      90      100     110     120
                                100     110     120     130     140     150
SEQ  REVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGH
      .....
SEQ  REVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGH
      130     140     150     160     170     180
                                160     170     180     190     200     210
SEQ  RGEHVLHLEPGSVESGRGRCPHEPSRPFASFIDGELYTGLTADFLGREAMIFRSGGPRP
      .....
SEQ  RGEHVLHLEPGSVESGRGRCPHEPSRPFASFIDGELYTGLTADFLGREAMIFRSGGPRP
      190     200     210     220     230     240
                                220     230     240     250     260     270
SEQ  ALRSDSDQSLLDHPRFVMAARI PENS DQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVC
      .....
SEQ  ALRSDSDQSLLDHPRFVMAARI PENS DQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVC
      250     260     270     280     290     300
                                280     290     300     310     320     330
SEQ  VNDAGGQRLVKNKWFSTFLKARLVCSVPGPGAETHFDQLEDVFLWPKAGKSLEVYALFS
      .....
SEQ  VNDAGGQRLVKNKWFSTFLKARLVCSVPGPGAETHFDQLEDVFLWPKAGKSLEVYALFS
      310     320     330     340     350     360
                                340     350     360     370     380     390
SEQ  TVSAVFQGFVAVCVYHMADIWEVFNGPFQHRDGPQHGWGPYGGKVFPFRPGVCPSKMTAQF
```

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      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  TVSAVFQGFVAVCVYHMAIWEVFNGPFAHRDGPQHGWGPYGGKVPFPRPGVCPSKMTAQP
      370          380          390          400          410          420

      400          410          420          430          440          450
SEQ  GRPFGSTKDYPDEVLQFARAHPLMFVPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  GRPFGSTKDYPDEVLQFARAHPLMFVPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGT
      430          440          450          460          470          480

      460          470          480          490          500          510
SEQ  YDVIFLGTDSGSLVKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGS
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  YDVIFLGTDSGSLVKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGS
      490          500          510          520          530          540

      520          530          540          550          560          570
SEQ  RLGVAQLRLHQCEYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  RLGVAQLRLHQCEYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNA
      550          560          570          580          590          600

      580          590          600          610          620          630
SEQ  LQCLGQSQEEEEAVGLVAATMVYGTGTEHNSTFLECLPKSPAAVRWLLQRPDQVKTDE
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  LQCLGQSQEEEEAVGLVAATMVYGTGTEHNSTFLECLPKSPAAVRWLLQRPDQVKTDE
      610          620          630          640          650          660

      640          650          660          670          680          690
SEQ  RVLHTEGRLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEE
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  RVLHTEGRLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEE
      670          680          690          700          710          720

      700          710          720          730          740          750
SEQ  PPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSTRSGKQAR
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  PPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSTRSGKQAR
      730          740          750          760          770          780

      760          770          780
SEQ  GKSAGLELGKKMKSRVHAENRTPREVEAT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ  GKSAGLELGKKMKSRVHAENRTPREVEAT
      790          800          810

```

781 residues in 1 query sequences

814 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Feb 10 16:26:11 2003 done: Mon Feb 10 16:26:12 2003

Scan time: 0.034 Display time: 0.866

Function used was FASTA